FIG. 1A

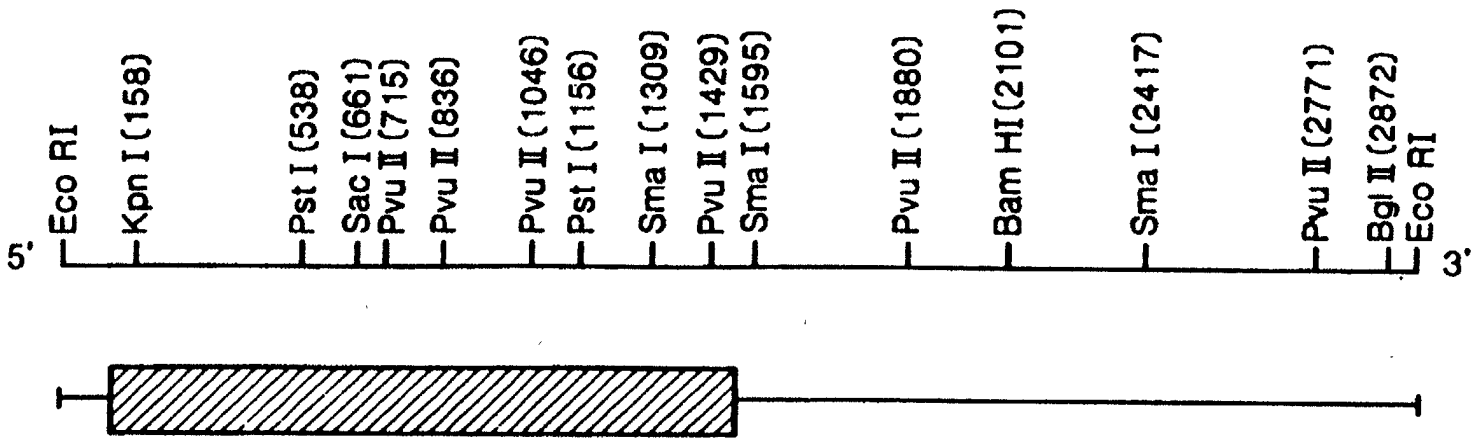


FIG. 1B-1

```
1   GCCATCTGGGCCCAGGCCCCATGCCCCGAGGAGGGGTGGTCTGAAGCCCACCAGAGCCCCCTGCCAGACTGTCTGCCTCCCTTCTGACTG

                1                              11                              21
                MetAlaSerAsnSerSerSerCysProThrProGlyGlyGlyHisLeuAsnGlyTyrProValProProTyrAlaPhe
91  TGGCCGCTTGGCATGGCCAGCAACAGCAGCTCCTGCCCGACACCTGGGGGCGGGCACCTCAATGGGTACCCGGTGCCTCCCTACGCCTTC

                31                             41                              51
    PhePheProProMetLeuGlyGlyLeuSerProProGlyAlaLeuThrThrLeuGlnHisGlnLeuProValSerGlyTyrSerThrPro
181 TTCTTCCCCCCTATGCTGGGTGGACTCTCCCCGCCAGGCGCTCTGACCACTCTCCAGCACCAGCTTCCAGTTAGTGGATATAGCACACCA

                61                             71                              81
    SerProAlaThrIleGluThrGlnSerSerSerSerGluGluIleValProSerProProSerProProProLeuProArgIleTyrLys
271 TCCCCAGCCACCATTGAGACCCAGAGCAGCAGTTCTGAAGAGATAGTGCCCAGCCCTCCCTCGCCACCCCCTCTACCCCGCATCTACAAG
```

FIG. 1B-2

```
                91                  101                 111
    ProCysPheValCysGlnAspLysSerSerGlyTyrHisTyrGlyValSerAlaCysGluGlyCysLysGlyPhePheArgArgSerIle
361 CCTTGCTTTGTCTGTCAGGACAAGTCCTCAGGCTACCACTATGGGGTCAGCGCCTGTGAGGGCTGCAAGGGCTTCTTCCGCCGCAGCATC

               121                 131                 141
    GlnLysAsnMetValTyrThrCysHisArgAspLysAsnCysIleIleAsnLysValThrArgAsnArgCysGlnTyrCysArgLeuGln
451 CAGAAGAACATGGTGTACACGTGTCACCGGGACAAGAACTGCATCATCAACAAGGTGACCCGGAACCGCTGCCAGTACTGCCGACTGCAG

               151                 161                 171
    LysCysPheGluValGlyMetSerLysGluSerValArgAsnAspArgAsnLysLysLysLysGluValProLysProGluCysSerGlu
541 AAGTGCTTTGAAGTGGGCATGTCCAAGGAGTCTGTGAGAAACGACCGAAACAAGAAGAAGAAGGAGGTGCCCAAGCCCGAGTGCTCTGAG

               181                 191                 201
    SerTyrThrLeuThrProGluValGlyGluLeuIleGluLysValArgLysAlaHisGlnGluThrPheProAlaLeuCysGlnLeuGly
631 AGCTACACGCTGACGCCGGAGGTGGGGGAGCTCATTGAGAAGGTGCGCAAAGCGCACCAGGAAACCTTCCCTGCCCTCTGCCAGCTGGGC

               211                 221                 231
    LysTyrThrThrAsnAsnSerSerGluGlnArgValSerLeuAspIleAspLeuTrpAspLysPheSerGluLeuSerThrLysCysIle
721 AAATACACTACGAACAACAGCTCAGAACAACGTGTCTCTCTGGACATTGACCTCTGGGACAAGTTCAGTGAACTCTCCACCAAGTGCATC

               241                 251                 261
    IleLysThrValGluPheAlaLysGlnLeuProGlyPheThrThrLeuThrIleAlaAspGlnIleThrLeuLeuLysAlaAlaCysLeu
811 ATTAAGACTGTGGAGTTCGCCAAGCAGCTGCCCGGCTTCACCACCCTCACCATCGCCGACCAGATCACCCTCCTCAAGGCTGCCTGCCTG

               271                 281                 291
    AspIleLeuIleLeuArgIleCysThrArgTyrThrProGluGlnAspThrMetThrPheSerAspGlyLeuThrLeuAsnArgThrGln
901 GACATCCTGATCCTGCGGATCTGCACGCGGTACACGCCCGAGCAGGACACCATGACCTTCTCGGACGGGCTGACCCTGAACCGGACCCAG

               301                 311                 321
    MetHisAsnAlaGlyPheGlyProLeuThrAspLeuValPheAlaPheAlaAsnGlnLeuLeuProLeuGluMetAspAspAlaGluThr
991 ATGCACAACGCTGGCTTCGGCCCCCTCACCGACCTGGTCTTTGCCTTCGCCAACCAGCTGCTGCCCCTGGAGATGGATGATGCGGAGACG

               331                 341                 351
    GlyLeuLeuSerAlaIleCysLeuIleCysGlyAspArgGlnAspLeuGluGlnProAspArgValAspMetLeuGlnGluProLeuLeu
1081 GGGCTGCTCAGCGCCATCTGCCTCATCTGCGGAGACCGCCAGGACCTGGAGCAGCCGGACCGGGTGGACATGCTGCAGGAGCCGCTGCTG
```

FIG. 1B-3

FIG. 2A

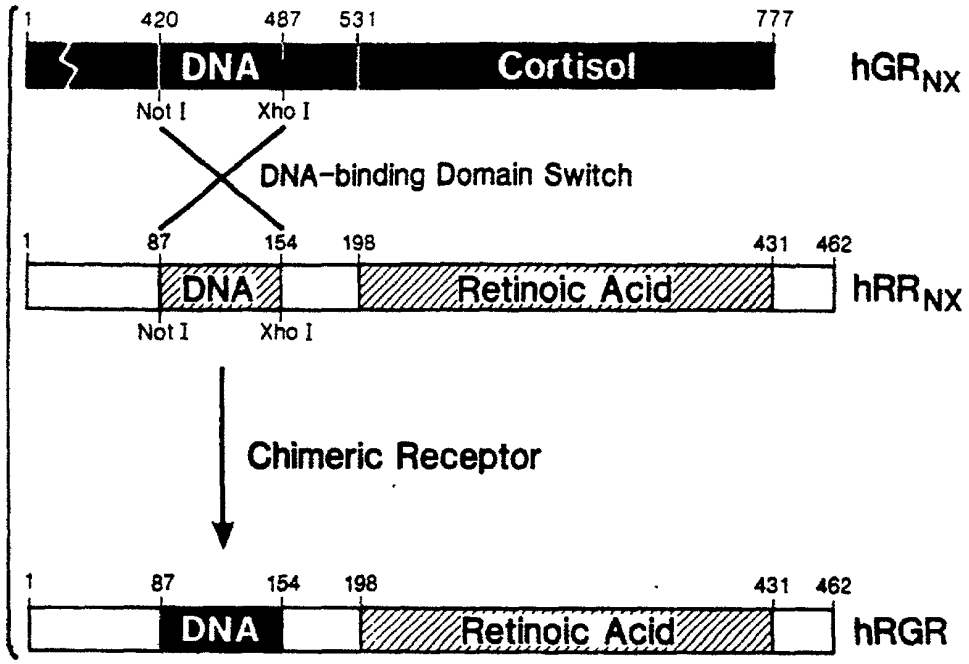

1
420
487
531
777
DNA
Cortisol
hGR$_{NX}$
Not I
Xho I
DNA-binding Domain Switch
1
87
154
198
431
462
DNA
Retinoic Acid
hRR$_{NX}$
Not I
Xho I
Chimeric Receptor
1
87
154
198
431
462
DNA
Retinoic Acid
hRGR

FIG. 2B

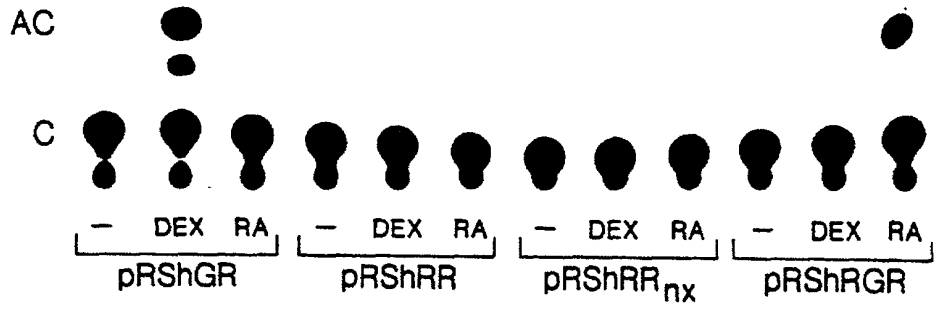

AC
C
–
DEX
RA
pRShGR
pRShRR
pRShRR$_{nx}$
pRShRGR

FIG. 3A

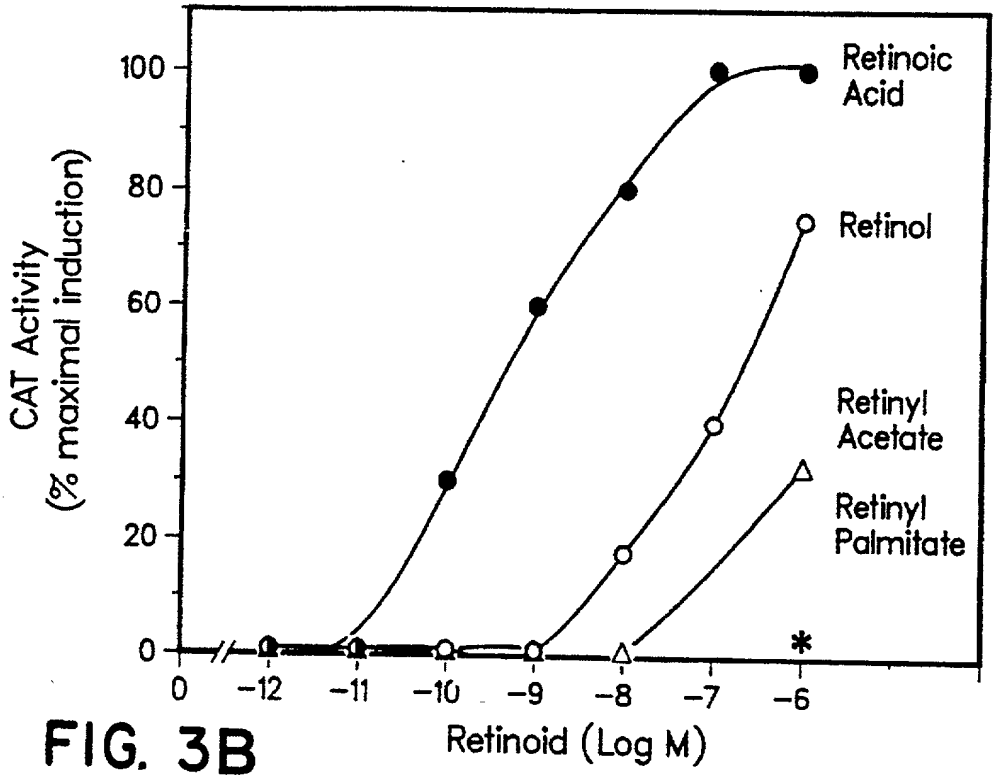

CAT Activity
(% maximal induction)
100
80
60
40
20
0
0
-12
-11
-10
-9
-8
-7
-6
Retinoic Acid
Retinol
Retinyl Acetate
Retinyl Palmitate
*
Retinoid (Log M)

FIG. 3B

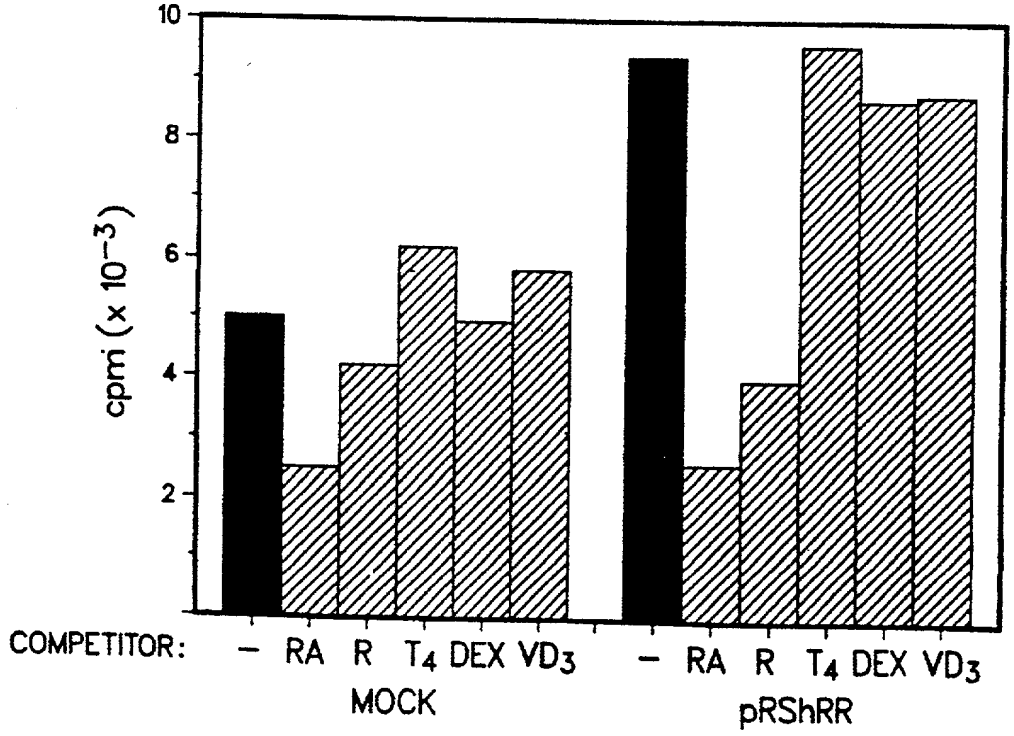

cpm (x 10⁻³)
10
8
6
4
2
COMPETITOR:
– RA R T4 DEX VD3
MOCK
– RA R T4 DEX VD3
pRShRR

FIG.4A

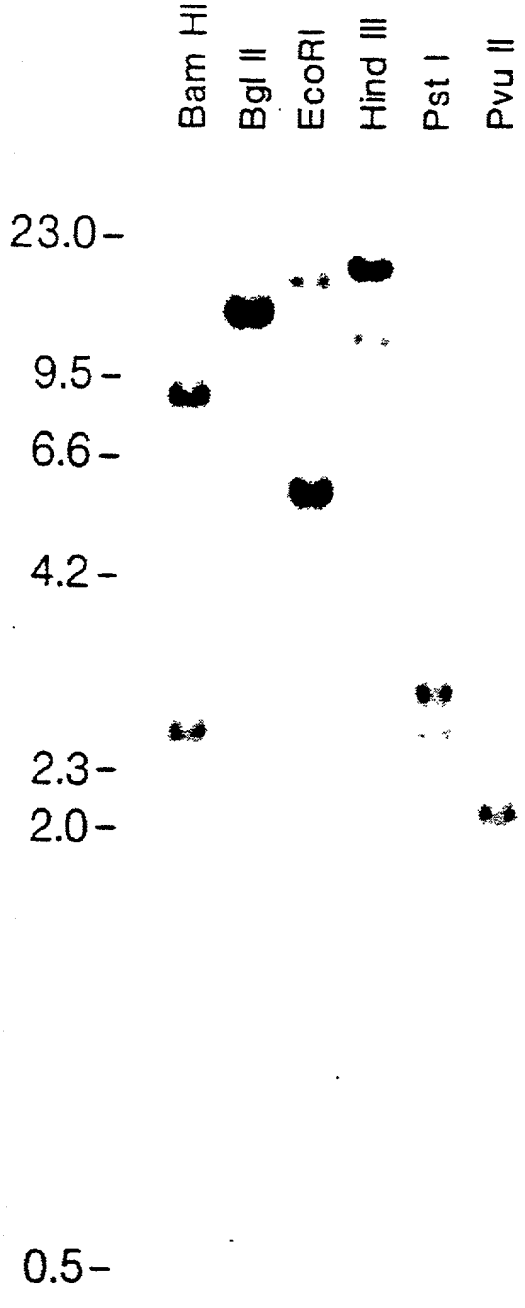
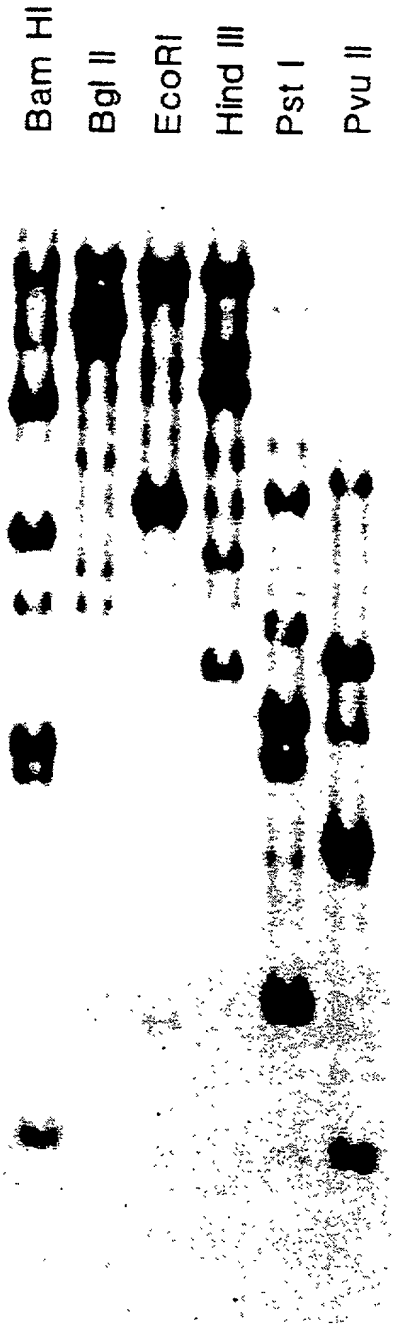

Bam HI
Bgl II
EcoRI
Hind III
Pst I
Pvu II
23.0-
9.5-
6.6-
4.2-
2.3-
2.0-
0.5-

FIG.4B


Bam HI
Bgl II
EcoRI
Hind III
Pst I
Pvu II

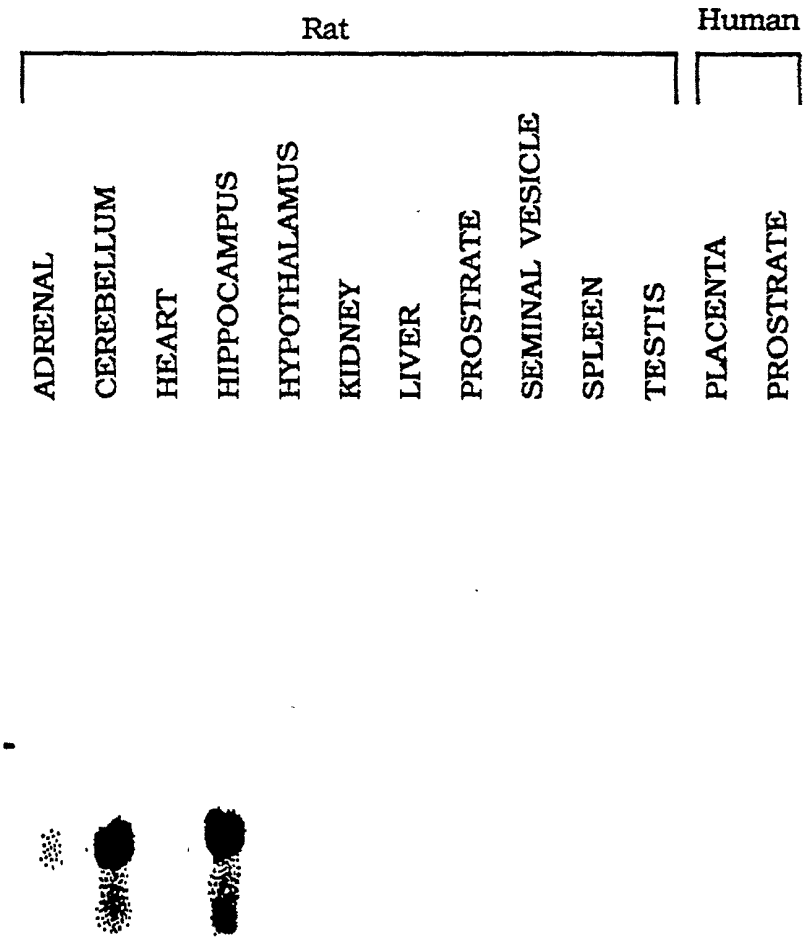

Rat
Human
ADRENAL
CEREBELLUM
HEART
HIPPOCAMPUS
HYPOTHALAMUS
KIDNEY
LIVER
PROSTRATE
SEMINAL VESICLE
SPLEEN
TESTIS
PLACENTA
PROSTRATE
28S -
18S -

FIGURE 5

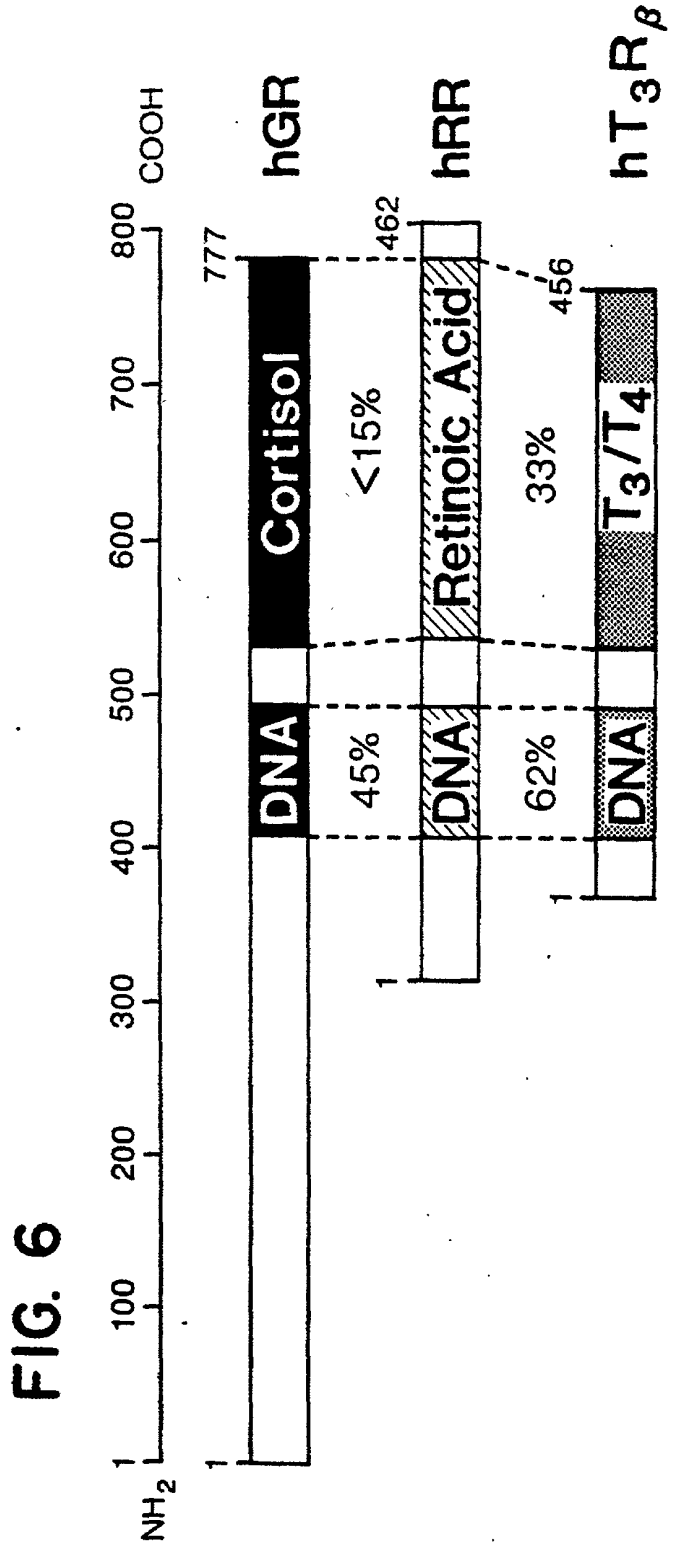

hGR
hRR
hT3Rβ
COOH
NH2
1
100
200
300
400
500
600
700
800
777
462
456
Cortisol
Retinoic Acid
T3/T4
DNA
DNA
DNA
<15%
33%
45%
62%

FIG. 6

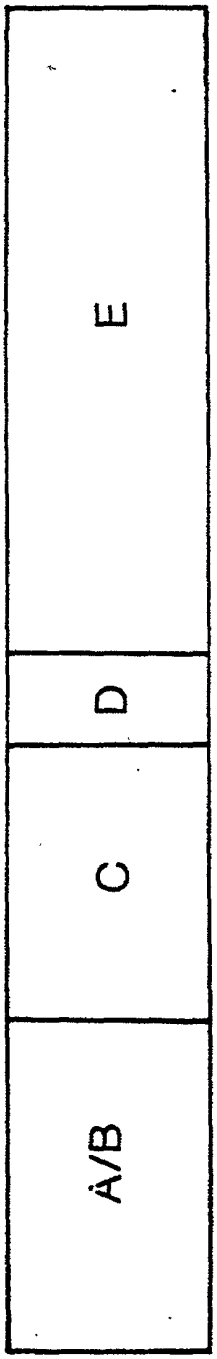


FIG. 7

FIG. 8-I

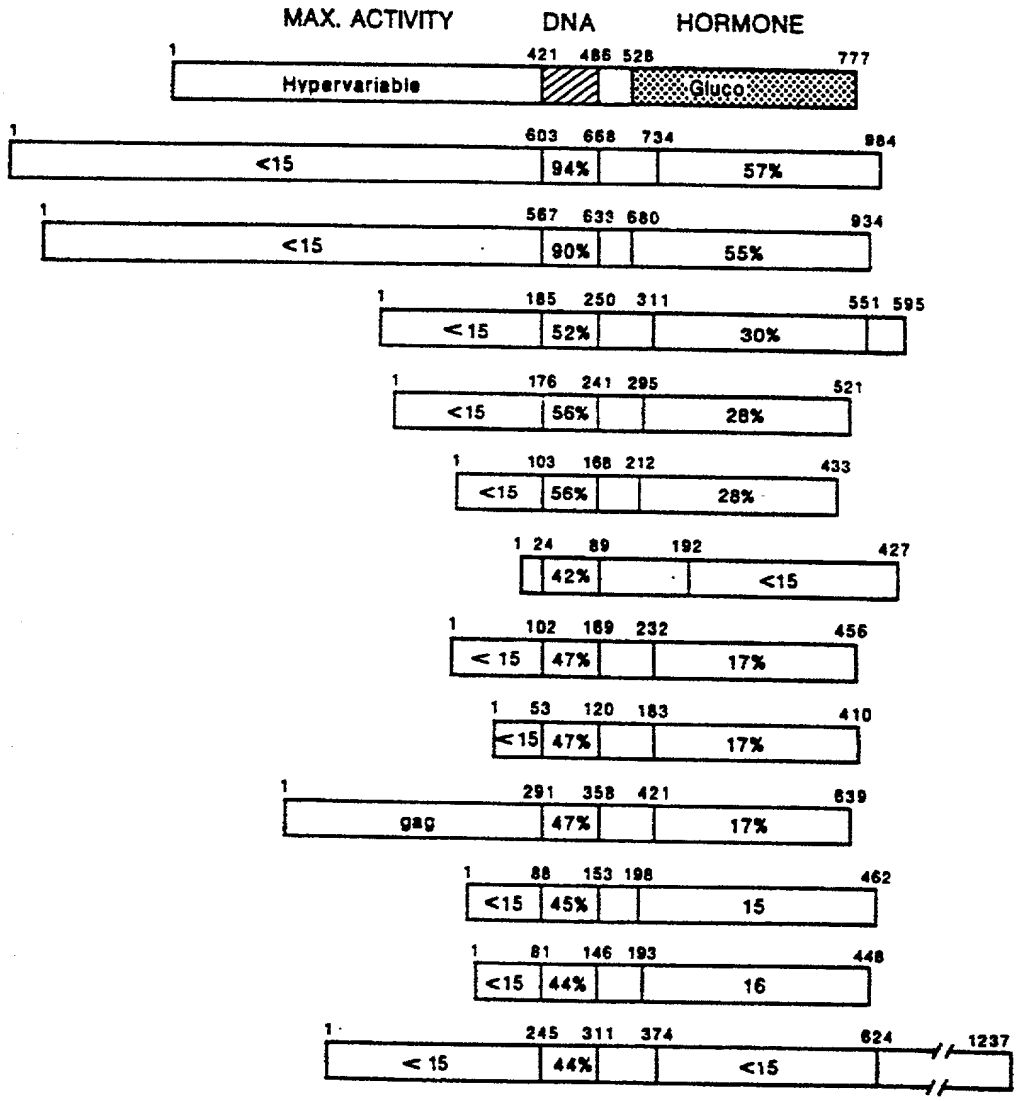
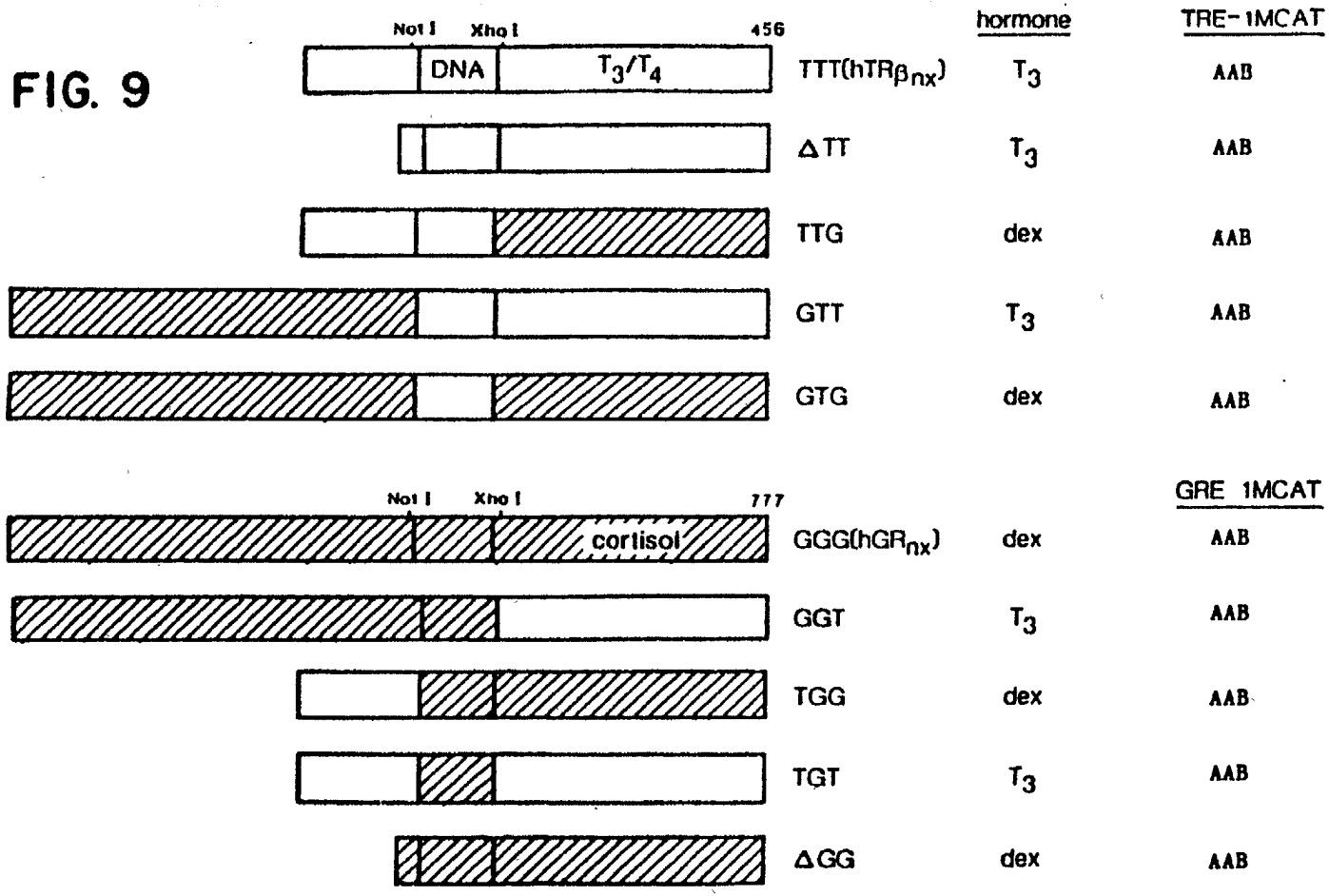

MAX. ACTIVITY
DNA
HORMONE
1
421 486 528
777
Hypervariable
Gluco
1
603 668 734
884
<15
94%
57%
1
567 633 680
934
<15
90%
55%
1
185 250 311
551 595
<15
52%
30%
1
176 241 295
521
<15
56%
28%
1
103 168 212
433
<15
56%
28%
1 24 89 192
427
42%
<15
1
102 169 232
456
<15
47%
17%
1
53 120 183
410
<15
47%
17%
1
291 358 421
639
gag
47%
17%
1
88 153 198
462
<15
45%
15
1
81 146 193
448
<15
44%
16
1
245 311 374
624
1237
<15
44%
<15

FIG. 8-2

	HRE	DNA BINDING	HORMONE BINDING IN VITRO	HORMONE BINDING IN VIVO	TRANS-ACTIVATION	CHROMO-SOME	SPECIES
GR	+[15-19]	+[16,17,21]	+[26,82]	+[48,52,77]	+[48,52,78,79]	5[26]	h,[26] r,[77] m,[78]
MR	nd	nd	nd	+[36]	+[36]	4[36]	h[36]
PR	+[24,34]	+[24,34]	nd	nd	+[34]	11[79]	rabbit,[32] h,[33] c,[34]
ER	+[22,23]	+[23,62]	nd	+[23,53,62]	+[53,62]	6[62]	h,[29] c,[30] frog[31]
ERR1	nd	nd	nd	nd	nd	nd	h[39]
ERR2	nd	nd	nd	nd	nd	nd	h[39]
VDR	nd	nd	nd	+[35]	nd	nd	h,[35] c[35]
T_3R_β	+[25]	+[25]	+[37]	nd	+[80]	3[37]	h[37]
T_3R_α	nd	nd	+[38,40]	nd	+[80]	17[40]	r,[40] h,[41] c[38]
V-erb A	+	+	(—)[38]	nd	nd	virus	c[28]
RAR	nd	nd	nd	+[42,43]	+[42,43]	17[83]	h[42,43]
HAP	nd	nd	nd	nd	nd	3[45]	h[45]
E75	nd	nd	nd	nd	nd		d[46]

FIG. 9



AAB = Activation Above Background